

XX	Sequence	1140 AA:	Db	961 DDSKERRNSLNRLFPKPKTIEFLERRRFGNTSALADDREFFYGLVWEGRETLIRLEDVRTP 1020
Query	Match	100.0% Score 5788; DB 22; length 1140;	Qy	1021 LLVRDAISESPDKGKMRNVVANVNGQIRPHVRDSESVESTATAEKADSSNKHWAPFA 1080
Best Local Similarity	100.0% Pred. No. 0;	Mismatches 0; Indels 0; Gaps 0;	Db	1021 LLVRDAISESPDKGKMRNVVANVNGQIRPHVRDSESVESTATAEKADSSNKHWAPFA 1080
Matches	1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	1 MSTHHSSTLPAFKKILVANRGEIARAFRALETAEGATVAYPRDRGSFHRSEAVR 60		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	1 MSTHHSSTLPAFKKILVANRGEIARAFRALETAEGATVAYPRDRGSFHRSEAVR 60			
Qy	61 IGTGESPVAYLDEIGAKKKYKADAYPGYGLSEANQLARECAGNITFGPTPEV 120			
Db	61 IGTGESPVAYLDEIGAKKKYKADAYPGYGLSEANQLARECAGNITFGPTPEV 120			
Qy	121 LDLTGDKSRAVTAKKAGLPVLAESTPSKNIETVKSABGQTYIFVKAVAGGGGRGMRF 180		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	121 LDLTGDKSRAVTAKKAGLPVLAESTPSKNIETVKSABGQTYIFVKAVAGGGGRGMRF 180		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	181 VASDELRLKATEASREADAAGFDCAVVTPNQHTEVOLGDHTCEVHLYERDGS 240		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	181 VASDELRLKATEASREADAAGFDCAVVTPNQHTEVOLGDHTCEVHLYERDGS 240		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	241 LQRHQKVYIAPQHDLPELRDRCADAVKFCRSIGYQAGTVEFLVNEKGNTVIEEN 300		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	241 LQRHQKVYIAPQHDLPELRDRCADAVKFCRSIGYQAGTVEFLVNEKGNTVIEEN 300		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	301 PRIQEVHTTEEVTLVLUKAQMLAAGATLKGLTQDKIKTHGALOCRITEDPN 360		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	301 PRIQEVHTTEEVTLVLUKAQMLAAGATLKGLTQDKIKTHGALOCRITEDPN 360		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	361 FRPDGTTIAYRSPGGAGYGRUDGAQQLGEITAHDMSMVKMTGRGSDTETAVARAQL 420		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	361 FRPDGTTIAYRSPGGAGYGRUDGAQQLGEITAHDMSMVKMTGRGSDTETAVARAQL 420		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	421 AEFTVSGVATNIGFLRALLREEDFTSKRATGFADHPLQAPADDQGRIDLQYALW 480		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	421 AEFTVSGVATNIGFLRALLREEDFTSKRATGFADHPLQAPADDQGRIDLQYALW 480		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	481 TUNKPHGVKRDVAPIDKLPNITDPLURGSRRLQKGPAARDLREQDALAVDTT 540		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	481 TUNKPHGVKRDVAPIDKLPNITDPLURGSRRLQKGPAARDLREQDALAVDTT 540		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	541 FRDAHQSLATRVSFAKLPAAEAVAKLTPPELSEVAWGSATYDVAMRFEDPDRDLE 600		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	541 FRDAHQSLATRVSFAKLPAAEAVAKLTPPELSEVAWGSATYDVAMRFEDPDRDLE 600		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	601 LREAMPVNVIQMLLGRGRNVTGVTYPPDSCTCRAFTKEAASSGVDFTRIEFLANDYSQMRPA 660		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	601 LREAMPVNVIQMLLGRGRNVTGVTYPPDSCTCRAFTKEAASSGVDFTRIEFLANDYSQMRPA 660		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	661 IDAVLETNTAVAEAMAYGSDLSPNEKLYTDLYKMAEETIVSGAHLAIKOMAGLR 720		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	661 IDAVLETNTAVAEAMAYGSDLSPNEKLYTDLYKMAEETIVSGAHLAIKOMAGLR 720		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	721 PAATVKAFLARLREDFLPVHVTHTAGGOLATVAAQAGADAVGASAPLSGTTSQ 780		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	721 PAATVKAFLARLREDFLPVHVTHTAGGOLATVAAQAGADAVGASAPLSGTTSQ 780		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	781 LSATVAAFLATRDRDGLSLEAVSDLEPYHEAVRGLYLPFESGTGPCTGRVYRHELPGOL 840		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	781 LSATVAAFLATRDRDGLSLEAVSDLEPYHEAVRGLYLPFESGTGPCTGRVYRHELPGOL 840		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	841 SNLRAQATLGLADLPEELDQYAVNEMGRPCKVTPPSKWKDGLALHVGACVDP 900		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	841 SNLRAQATLGLADLPEELDQYAVNEMGRPCKVTPPSKWKDGLALHVGACVDP 900		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	901 AADPQKYDTPDSVIAFLRSLGNPGWBPRLTRAEGSEKGAPLVEPEOAHLD 960		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Db	901 AADPQKYDTPDSVIAFLRSLGNPGWBPRLTRAEGSEKGAPLVEPEOAHLD 960		Db	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	961 DDSKERRNSLNRLFPKPKTIEFLERRRFGNTSALADDREFFYGLVWEGRETLIRLEDVRTP 1020		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140
Qy	121 LDLTGDKSRAVTAKKAGLPVLAESTPSKNIETVKSABGQTYIFVKAVAGGGGRGMRF 180		Qy	1081 GWVTTVAEGDEVKAGDAVIAEAMKMEATITASDGKIDRVVPPATKVEGGDLIVWS 1140

Db	121	LDTGGDKSRAVAAKKAGLPLVLAESTPSKNIDEIVKSAEQGTYPIFVKAAGGGGRGMRF	180	XX
QY	181	VASPDRLKLTAEASREAEAAFGDGWYVERAVINPQHTEVQIQLGDHGEWVHLYRDCS	240	DT 27-AUG-2002 (first entry)
Db	181	VASPDRLKLTAEASREAEAAFGDGWYVERAVINPQHTEVQIQLGDHGEWVHLYRDCS	240	DE Corynebacterium wild-type feedback-resistant pyruvate carboxylase enzyme.
QY	241	LQRHQKVEIAPAQHLDPELDRICADAVFKCRSIGQGAGTVEFLVDEKGHVFLEM	300	XX
Db	241	LQRHQKVEIAPAQHLDPELDRICADAVFKCRSIGQGAGTVEFLVDEKGHVFLEM	300	DE Corynebacterium wild-type feedback-resistant pyruvate carboxylase enzyme;
QY	301	PRLOVEHTVTEEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRTTEDPN	360	KW Feedback-resistant; pyruvate carboxylase; enzyme; aspartic acid feedback inhibition resistant.
Db	301	PRLOVEHTVTEEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRTTEDPN	360	OS Corynebacterium glutamicum.
QY	361	FRPDTGTTAYRSPPGGAGRGLDQAGLGEITAHFDSMVKMTCRGSDEETAVARAQL	420	XX
Db	361	FRPDTGTTAYRSPPGGAGRGLDQAGLGEITAHFDSMVKMTCRGSDEETAVARAQL	420	OS Corynebacterium glutamicum.
QY	421	AEFTVSGVATNIGFLRALLREDEFTSKRATGTFADPHLQAPPADDEQRLDYLADV	480	XX
Db	421	AEFTVSGVATNIGFLRALLREDEFTSKRATGTFADPHLQAPPADDEQRLDYLADV	480	DE Corynebacterium glutamicum.
QY	481	TWNKPHGFRPKDVAAPIDKLPNKLDPFLRGSRDLQPGAAFARDLREQDALAVDT	540	XX
Db	481	TWNKPHGFRPKDVAAPIDKLPNKLDPFLRGSRDLQPGAAFARDLREQDALAVDT	540	DE Corynebacterium glutamicum.
QY	541	FRDHQSLIATRVSFALKPAAAVAKLTPELLSVEAWGATDVAMRFLFEDPWDRLDE	600	XX
Db	541	FRDHQSLIATRVSFALKPAAAVAKLTPELLSVEAWGATDVAMRFLFEDPWDRLDE	600	DE Corynebacterium glutamicum.
QY	601	LREAMPNTNIQMLLGRGNTWGVYPDPDSWCRAFKEAASGVDIFRFDALNDVSQMRPA	660	XX
Db	601	LREAMPNTNIQMLLGRGNTWGVYPDPDSWCRAFKEAASGVDIFRFDALNDVSQMRPA	660	DE Corynebacterium glutamicum.
QY	661	IDAVLETTVAVAVAMAYSGDLSDPNEKLYTDLYKMAELVKGASHILATKDMAGLLR	720	XX
Db	661	IDAVLETTVAVAVAMAYSGDLSDPNEKLYTDLYKMAELVKGASHILATKDMAGLLR	720	DE Corynebacterium glutamicum.
QY	721	PAAVTKLVTALRREFDLPVHVIHTDAGGQATYFAAQAGADAVGASAPLGSQTSSQPS	780	XX
Db	721	PAAVTKLVTALRREFDLPVHVIHTDAGGQATYFAAQAGADAVGASAPLGSQTSSQPS	780	DE Corynebacterium glutamicum.
QY	781	LSATVAAFAHTRDRDGTLSEAVSDLEPYWEAVRGGLYLFPESTGPGTGRVYRHEIPCGQL	840	XX
Db	781	LSATVAAFAHTRDRDGTLSEAVSDLEPYWEAVRGGLYLFPESTGPGTGRVYRHEIPCGQL	840	DE Corynebacterium glutamicum.
QY	841	SNRQAQATAGLADRFELIEDVAVVEMGLGPKTPKPSKVGDLALHVGAGVDPAD	900	XX
Db	841	SNRQAQATAGLADRFELIEDVAVVEMGLGPKTPKPSKVGDLALHVGAGVDPAD	900	DE Corynebacterium glutamicum.
QY	901	AADPKDIDPSVIAFLRGELGNPPGGWPEPLRTRALEGSRSGKAPLTVPEEEQAHDA	960	XX
Db	901	AADPKDIDPSVIAFLRGELGNPPGGWPEPLRTRALEGSRSGKAPLTVPEEEQAHDA	960	DE Corynebacterium glutamicum.
QY	961	DDSKERRNSLNRLFPKPTTEFLERHRFRGNTSALDREFFYGLVGERETLRLPDRPT	1020	XX
Db	961	DDSKERRNSLNRLFPKPTTEFLERHRFRGNTSALDREFFYGLVGERETLRLPDRPT	1020	DE Corynebacterium glutamicum.
QY	1021	LAVRLDAISEPDGKGMVNWVANNGQIIPMRVDRDSVSYVATAEADSNKGVHVAPEA	1080	XX
Db	1021	LAVRLDAISEPDGKGMVNWVANNGQIIPMRVDRDSVSYVATAEADSNKGVHVAPEA	1080	DE Corynebacterium glutamicum.
QY	1081	GVWTWVAGDEVKAGDAVIAEAMMNEATIASVGDKIDRVVVPATKVGDDLIWVVS	1140	XX
Db	1081	GVWTWVAGDEVKAGDAVIAEAMMNEATIASVGDKIDRVVVPATKVGDDLIWVVS	1140	DE Corynebacterium glutamicum.
RESULT 4	181	VASPDRLKLTAEASREAEAAFGDGWYVERAVINPQHTEVQIQLGDHGEWVHLYRDCS	240	XX
AAU98053	181	VASPDRLKLTAEASREAEAAFGDGWYVERAVINPQHTEVQIQLGDHGEWVHLYRDCS	240	DE Corynebacterium glutamicum.
ID	181	VASPDRLKLTAEASREAEAAFGDGWYVERAVINPQHTEVQIQLGDHGEWVHLYRDCS	240	OS Corynebacterium glutamicum.
XX	181	VASPDRLKLTAEASREAEAAFGDGWYVERAVINPQHTEVQIQLGDHGEWVHLYRDCS	240	XX
AC	181	VASPDRLKLTAEASREAEAAFGDGWYVERAVINPQHTEVQIQLGDHGEWVHLYRDCS	240	OS Corynebacterium glutamicum.
AC	AAU98053;	AAU98053;	AAU98053;	XX

The present invention relates to a new mutated, feedback-resistant pyruvate carboxylase enzyme. The invention is useful for producing an amino acid (e.g., L-Tyr, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino acid from the medium. The vector of the invention is useful for replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first recombinant strain, and replacing the selectable marker gene in the first recombinant strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback-resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic acid. The present amino acid sequence represents the wild-type feedback-resistant pyruvate carboxylase enzyme of the invention.

CC Disclosure: Fig 2; 42pp; English.

CC (ARCHER) ARCHER-DANIELS MIDLAND CO.

CC PT Hanke PD;

CC DR WPI; 2002-463267/49.

CC PT Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-Lysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and L-isoleucine

CC PT Disclosure: Fig 2; 42pp; English.

The present invention relates to a new mutated, feedback-resistant pyruvate carboxylase enzyme. The invention is useful for producing an amino acid (e.g., L-Tyr, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino acid from the medium. The vector of the invention is useful for replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first recombinant strain, and replacing the selectable marker gene in the first recombinant strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback-resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic acid. The present amino acid sequence represents the wild-type feedback-resistant pyruvate carboxylase enzyme of the invention.

CC Sequence 1140 AA;

CC Query Match 100.0%; Score 5788; DB 23; Length 1140;

CC Best Local Similarity 100.0%; Pred. No. 0;

CC Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC

Db	241	LQRHQKVVEIAPAQHLDPELDRICADAQFCRSIGYQAGTVEFLVDEKGNHFIEMN	XX
Qy	301	PRIQVENTTVEETVENDVLAQMRAGATKEGLTQDKKTHAALOCRITEDPNN	PN
Db	301	PRIQVENTTVEETVENDVLAQMRAGATKEGLTQDKKTHAALOCRITEDPNN	XX
Qy	361	FRPDGTITAYRSPGGAGVRLDGAQLGGEITAHDMSLYKMTGCRGSDETAVARQRAL	PD
Db	361	FRPDGTITAYRSPGGAGVRLDGAQLGGEITAHDMSLYKMTGCRGSDETAVARQRAL	XX
Qy	421	AEFTVSGVATNIGFLRALLREEDFTSKRATGFIAHDPHLQAPPADDEGRLILYADV	PR
Db	421	AEFTVSGVATNIGFLRALLREEDFTSKRATGFIAHDPHLQAPPADDEGRLILYADV	XX
Db	421	AEFTVSGVATNIGFLRALLREEDFTSKRATGFIAHDPHLQAPPADDEGRLILYADV	23-DEC-1998; 98WO-US27301.
Qy	481	TVNPKPHGVPKDVAQPKDQPLRGSRSRDLQGPAAFRDRLRQDADLVATD'T	XX
Db	481	TVNPKPHGVPKDVAQPKDQPLRGSRSRDLQGPAAFRDRLRQDADLVATD'T	23-DEC-1998; 98WO-US27301.
Qy	541	FRDAHQSLATRVRASFAKLPKAEEAVAKLPELSSVEAWGATYDAMARLFEDPWRDDE	PA
Db	541	FRDAHQSLATRVRASFAKLPKAEEAVAKLPELSSVEAWGATYDAMARLFEDPWRDDE	(SINS/;) SINSKEY A. J.
Qy	601	LREAMPVNITQMLLRGRNTVGYTPYPSDSCRAFYKEAASSGVDIFRIFALNDYSQMRPA	PA
Db	601	LREAMPVNITQMLLRGRNTVGYTPYPSDSCRAFYKEAASSGVDIFRIFALNDYSQMRPA	(LESS/) LESSARD P. A.
Qy	661	IDAVLETNTAAEVAMAYSSGDLSDPNEKLYTDLYKLKMAETEVKGSAHLIAIKDMAGLLR	PA
Db	661	IDAVLETNTAAEVAMAYSSGDLSDPNEKLYTDLYKLKMAETEVKGSAHLIAIKDMAGLLR	(WILL/) WILLIS L. B.
Qy	721	PAATVTKLVALRREDFLPVHHTDTAGQLATVFAAQAGADAVGASAPLSETTSQPS	XX
Db	721	PAATVTKLVALRREDFLPVHHTDTAGQLATVFAAQAGADAVGASAPLSETTSQPS	XX
Qy	781	LSATVAAFAHTTRDGLSEAVSDLEPYEAVRGLYLPFESGTFCPTGVRHIPPGL	PT
Db	781	LSATVAAFAHTTRDGLSEAVSDLEPYEAVRGLYLPFESGTFCPTGVRHIPPGL	Sinkey AJ, Lessard PA, Willis LB;
Qy	841	SNLRQATATLGLADRFELLEDNYAVNEMLGRPTKVTSPSKWVGDALILVGASVDPAF	XX
Db	841	SNLRQATATLGLADRFELLEDNYAVNEMLGRPTKVTSPSKWVGDALILVGASVDPAF	WPI: 2000-465746/40.
Qy	901	AADPOKYDPPDSVIAFLRQELGNPGWAEPLRRALESEGRSEGKAPLTYPEEQAHD	DR
Db	901	AADPOKYDPPDSVIAFLRQELGNPGWAEPLRRALESEGRSEGKAPLTYPEEQAHD	N-PSDB; AAA47533.
Qy	961	DDSKERRNSINLRFLPKPTEFLEHRRGNTSALDDRFYFGLVEGRFLIRLPDVRTP	XX
Db	961	DDSKERRNSINLRFLPKPTEFLEHRRGNTSALDDRFYFGLVEGRFLIRLPDVRTP	XX
Qy	1021	LLVRIDATESPDDKGMRNNTAVNGQIRPMVRDRSVESTATAEKADSSNKGHVAAPPA	Sequence 1141 AA:
Db	1021	LLVRIDATESPDDKGMRNNTAVNGQIRPMVRDRSVESTATAEKADSSNKGHVAAPPA	Query Match 99 %; Score 5784; DB 21; Length 1141;
Qy	1081	GWVWTVGAGDDEVAGDAYAIEAMKMENTITASVGDKIDRVVPAATKVEGGDLIVWS	Best Local Similarity 99 %; Pred. No. 0; Matches 1139; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db	1081	GWVWTVGAGDDEVAGDAYAIEAMKMENTITASVGDKIDRVVPAATKVEGGDLIVWS	Query 1 MSTHSSSTLPAFKKIVLVAHNGEIAWRAFRALETOATAIYPREDRGSFHSFASEAVR
Qy	1081	GWVWTVGAGDDEVAGDAYAIEAMKMENTITASVGDKIDRVVPAATKVEGGDLIVWS	Db 2 VSTHSSSTLPAFKKIVLVAHNGEIAWRAFRALETOATAIYPREDRGSFHSFASEAVR
Qy	1241	LQRHQKVVEIAPAQHLDPELDRICADAQFCRSIGYQAGTVEFLVDEKGNHFIEMN	61
Db	1241	LQRHQKVVEIAPAQHLDPELDRICADAQFCRSIGYQAGTVEFLVDEKGNHFIEMN	121
Qy	301	PRIQVENTTVEETVENDVLAQMRAGATKEGLTQDKKTHAALOCRITEDPNN	180
Db	301	PRIQVENTTVEETVENDVLAQMRAGATKEGLTQDKKTHAALOCRITEDPNN	181
Qy	361	FRPDGTITAYRSPGGAGVRLDGAQLGGEITAHDMSLYKMTGCRGSDETAVARQRAL	181
Db	361	FRPDGTITAYRSPGGAGVRLDGAQLGGEITAHDMSLYKMTGCRGSDETAVARQRAL	182
Qy	421	AEFTVSGVATNIGFLRALLREEDFTSKRATGFIAHDPHLQAPPADDEGRLILYADV	240
Db	421	AEFTVSGVATNIGFLRALLREEDFTSKRATGFIAHDPHLQAPPADDEGRLILYADV	241
Qy	481	TVNPKPHGVPKDVAQPKDQPLRGSRSRDLQGPAAFRDRLRQDADLVATD'T	241
Db	481	TVNPKPHGVPKDVAQPKDQPLRGSRSRDLQGPAAFRDRLRQDADLVATD'T	242
Qy	541	TVNPKPHGVPKDVAQPKDQPLRGSRSRDLQGPAAFRDRLRQDADLVATD'T	242
Db	541	TVNPKPHGVPKDVAQPKDQPLRGSRSRDLQGPAAFRDRLRQDADLVATD'T	242
OS	OS	Corynebacterium glutamicum.	W020039305-A1.

QY	541 FRDAHQSLLATRVRSEALKPAEAVALTPELSSVEANGATYDVMARLFEDPWDRLDE 600	PT Increasing microbial production of specific amino acids by
Db	542 FRDAHQSLLATRVRSEALKPAEAVALTPELSSVEANGATYDVMARLFEDPWDRLDE 601	PT Increasing activity or expression of pyruvate carboxylase
QY	601 LREAMPVNNTQMLLRGRNTVGTYPYPSVCRAYKEAASSGVDIFRFDALNDVSQMRPA 660	XX
Db	602 LREAMPVNNTQMLLRGRNTVGTYPYPSVCRAYKEAASSGVDIFRFDALNDVSQMRPA 661	XX
QY	661 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLYKMAEETVKSGAHLAIKDMAGLRL 720	CC This invention describes the isolation of a pyruvate carboxylase from corynebacterium glutamicum which is used in a novel method for
Db	662 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLYKMAEETVKSGAHLAIKDMAGLRL 721	CC production of lysine, threonine, homoserine, glutamate and/or arginine, CC variously useful as feed additives, condiments, pharmaceuticals and CC intermediates for fine chemicals. Increasing pyruvate carboxylase activity increases the yield of microbial production of amino acids CC of the aspartate and/or glutamate families, e.g. about 50% more lysine, CC 40% more threonine and 150% more homoserine are secreted into the CC culture medium.
QY	721 PAAVTKLVTALARREFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 780	XX
Db	722 PAAVTKLVTALARREFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 781	XX
QY	781 LSA1VAFAHTRRTDTGLSLEAVSDLEYWEAVRGLYLPFESSTPGPGVRHEIPEGQL 840	SQ Sequence 1140 AA;
Db	782 LSA1VAFAHTRRTDTGLSLEAVSDLEYWEAVRGLYLPFESSTPGPGVRHEIPEGQL 841	Query Match 99.9%; Score 5782; DB 20; Length 1140;
QY	841 SNLRAQATAGLADRFLFELIDNYAANVNMMLGRPTKVPSKVGVDIALHLVAGVDPADF 900	Best Local Similarity 99.9%; pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Db	842 SNLRAQATAGLADRFLFELIDNYAANVNMMLGRPTKVPSKVGVDIALHLVAGVDPADF 901	Matches 1139; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	901 AADPKDIDPSVIAFLRGELGNPPGGWPEPLTRALEGRSGKAPLTVFEEQAHLD 960	Db 61 1 MSHTGSTLPAFKKLYVANRGEIAVRAFRALETGATVATYPREDRGSFHSFASEAVR 60
Db	902 AADPKDIDPSVIAFLRGELGNPPGGWPEPLTRALEGRSGKAPLTVFEEQAHLD 961	Db 61 1 MSHTGSTLPAFKKLYVANRGEIAVRAFRALETGATVATYPREDRGSFHSFASEAVR 60
QY	961 DDKERKNSLNLLFLPKPTEELERHRFRGNSALDREFFYGLVKGRETILRLPVRTP 1020	Db 121 LDLTGOKSRVATAKAGLGPLVIAESTPSKNIDETIVSAEGOTYPTIFVKAVAGGGGRGMRF 180
Db	962 DDKERKNSLNLLFLPKPTEELERHRFRGNSALDREFFYGLVKGRETILRLPVRTP 1021	Db 121 LDLTGOKSRVATAKAGLGPLVIAESTPSKNIDETIVSAEGOTYPTIFVKAVAGGGGRGMRF 180
QY	1021 LIVRLDAISEPDKGMHNRVANVNGQIRPMVRDRSVESTVATAEADSNKGHVAPEA 1080	QY 181 VASPDRLKLAETEASBAAFGDGVYVERAVINHOIEVOLIGDHTGEVWHLXERDCS 240
Db	1022 LIVRLDAISEPDKGMHNRVANVNGQIRPMVRDRSVESTVATAEADSNKGHVAPEA 1081	Db 181 VASPDRLKLAETEASBAAFGDGVYVERAVINHOIEVOLIGDHTGEVWHLXERDCS 240
QY	1081 GIVWTWTAEGDVKAGDAVIAEAMMEATATASVCKDIDWVWPAATKVGGLLIVWVS 1140	QY 241 LQRHHOKVETAPAOHLDPELDRICADAVFKCRSGTYQAGTVERFLDEKGHNHYTEMN 300
Db	1082 GIVWTWTAEGDVKAGDAVIAEAMMEATATASVCKDIDWVWPAATKVGGLLIVWVS 1141	Db 241 LQRHHOKVETAPAOHLDPELDRICADAVFKCRSGTYQAGTVERFLDEKGHNHYTEMN 300
RESULT 6		
AAW93971	AAW93971 standard; protein; 1140 AA.	QY 301 PRIQVHVTYHETVTDLVKQMLLAGATKELGJTDQKIKTHGALQCRITEDPNNG 360
XX		Db 301 PRIQVHVTYHETVTDLVKQMLLAGATKELGJTDQKIKTHGALQCRITEDPNNG 360
AC		QY 361 FRPDGTITAYRSPGGAGVRLDGAQDQGETTAHFDMSLYKMTCRGSDFETAVARQL 420
DT	30-JUN-1999 (first entry)	Db 361 FRPDGTITAYRSPGGAGVRLDGAQDQGETTAHFDMSLYKMTCRGSDFETAVARQL 420
XX	C. glutamicum Pyruvate carboxylase protein.	QY 421 AEFTVSGVATNIGFLKALLREEDFTSKRIFTADPHLQAPPADDEGRILYLDADV 480
DE		Db 421 AEFTVSGVATNIGFLKALLREEDFTSKRIFTADPHLQAPPADDEGRILYLDADV 480
XX	Pyruvate carboxylase; amino acid production; lysine production; threonine production; homoserine production; glutamate production; arginine production; feed additive; condiment; pharmaceutical; fine chemical; ss.	QY 481 TYNKPGRPKDVAAPIDKPNIKDPLPGSDRDKLQKGPAAFARLDRQDQLAWTPT 540
OS	Corynebacterium glutamicum.	Db 481 TYNKPGRPKDVAAPIDKPNIKDPLPGSDRDKLQKGPAAFARLDRQDQLAWTPT 540
XX	DE19831609-A1.	QY 541 FRDAHQSLLATRVRSEALKPAEAVALTPELSSVEANGATYDVMARLFEDPWDRLDE 600
PD	15-APR-1999.	Db 541 FRDAHQSLLATRVRSEALKPAEAVALTPELSSVEANGATYDVMARLFEDPWDRLDE 600
XX		QY 601 LREAMPVNNTQMLLRGRNTVGTYPYPSVCRAYKEAASSGVDIFRFDALNDVSQMRPA 660
PF	14-JUL-1998; 98DE-1031609.	Db 601 LREAMPVNNTQMLLRGRNTVGTYPYPSVCRAYKEAASSGVDIFRFDALNDVSQMRPA 660
XX		QY 661 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLYKMAEETVKSGAHLAIKDMAGLRL 720
PR	04-OCT-1997; 97DE-1043894.	Db 661 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLYKMAEETVKSGAHLAIKDMAGLRL 720
XX		QY 721 PAAVTKLVTALARREFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 780
PA	(KERJ) FORSCHUNGZENTRUM JUELICH GMBH.	QY 721 PAAVTKLVTALARREFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 780
XX		QY 661 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLYKMAEETVKSGAHLAIKDMAGLRL 720
PI	Eikmanns B, Peters-Wendisch P, Sahn H;	Db 661 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLYKMAEETVKSGAHLAIKDMAGLRL 720
XX		QY 721 PAAVTKLVTALARREFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 780
DR	WPI: 1999-245521/21.	Db 721 PAAVTKLVTALARREFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 780
XX	N-PSDB; AAX24102.	Db 721 PAAVTKLVTALARREFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 780

QY	781	LSAIVAAFAATPRDQGLSLAEVDIPEPYEAVRGYLPLPESGTCPPTGRVYRHELPGCOL	840	CC
Db	781	LSAIVAAFAATPRDQGLSLAEVDIPEPYEAVRGYLPLPESGTCPPTGRVYRHELPGCOL	840	CC
Db	841	SNLRQQATAGLADRELIEDNYAVAVNEMIGRPTKVTPSSKVVGDLALHIVAGVDPAF	900	CC
Db	841	SNLRQQATAGLADRELIEDNYAVAVNEMIGRPTKVTPSSKVVGDLALHIVAGVDPAF	900	CC
QY	901	AADPQKYDIPDSVIAFLRGLGEGLGNPGGWPEPLRTHALEGSEGKAPLTVPEEEQAHLD	960	CC
QY	901	AADPQKYDIPDSVIAFLRGLGEGLGNPGGWPEPLRTHALEGSEGKAPLTVPEEEQAHLD	960	CC
Db	961	DDSKRRNSUNRLFPKPFEEFLRRRRENTSALLDREFFYGLVEGRELLIRLPDVRP	1020	CC
Db	961	DDSKRRNSUNRLFPKPFEEFLRRRRENTSALLDREFFYGLVEGRELLIRLPDVRP	1020	CC
QY	1021	LLVRDIASEPPDKKMRNVANVNGQIRPMVRDVSVESTATRKAQDSSNKGHAAAPFA	1080	CC
Db	1021	LLVRDIASEPPDKKMRNVANVNGQIRPMVRDVSVESTATRKAQDSSNKGHAAAPFA	1080	CC
QY	1081	GVVTVTVAEGDEVKAGDAVIAEAMKMEATASVDGKIDRUVVVAATKVEGGDILWVS	1140	CC
Db	1081	GVVTVTVAEGDEVKAGDAVIAEAMKMEATASVDGKIDRUVVVAATKVEGGDILWVS	1140	CC
QY	901	AADPQKYDIPDSVIAFLRGLGEGLGNPGGWPEPLRTHALEGSEGKAPLTVPEEEQAHLD	960	CC
QY	961	DDSKRRNSUNRLFPKPFEEFLRRRRENTSALLDREFFYGLVEGRELLIRLPDVRP	1020	CC
Db	961	DDSKRRNSUNRLFPKPFEEFLRRRRENTSALLDREFFYGLVEGRELLIRLPDVRP	1020	CC
RESULT 7				
ID	AAG93249	standard; Protein; 1140 AA.		
XX	AAG93249;			
AC	AAG93249;			
XX				
DT	26-SEP-2001	(first entry)		
DE	C glutamicum	protein fragment mutant P458S.		
XX				
KW	Coryneform	bacterium; amino acid synthesis; vitamin; saccharide;		
KW	organic	acid synthesis; mutant; mutein.		
XX				
OS	Corynebacterium	glutamicum.		
OS	Synthetic.			
XX				
KEY		Location/Qualifiers		
FT	Misc-difference 458			
FT	/note= " wild-type Pro substituted by Ser"			
XX	EP1108790-A2.			
PN				
XX	20-JUN-2001.			
PD				
XX	18-DEC-2000; 2000EP-0127688.			
PR	16-DEC-1999; 99JP-037484.			
PR	07-APR-2000; 2000JP-0159162.			
PR	03-AUG-2000; 2000JP-0269988.			
XX				
PA	(KYOW) KYOWA HAKKO KK.			
XX				
PI	Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;			
PI	Tateishi N, Senoh A, Ikeda M, Ozaki A;			
XX				
DR	WPI: 2001-376931/40.			
XX				
PT	Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene			
PT	are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and			
PS	Claim 43; Page -; 246PP + Sequence Listing; English.			
XX				
CC	The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium <i>Corynebacterium glutamicum</i> . These are useful for identifying the mutation point of a gene derived from a			
CC	mutant of coryneform bacterium, measuring expression amount and			
QY	781	LSAIVAAFAATPRDQGLSLAEVDIPEPYEAVRGYLPLPESGTCPPTGRVYRHELPGCOL	840	CC
Db	781	LSAIVAAFAATPRDQGLSLAEVDIPEPYEAVRGYLPLPESGTCPPTGRVYRHELPGCOL	840	CC
Db	721	PAAVKLVLTARREDFLPVWHTHTAGGDLATYFAAOAGADAVGASAPLSGTQS	780	CC
Db	721	PAAVKLVLTARREDFLPVWHTHTAGGDLATYFAAOAGADAVGASAPLSGTQS	780	CC
QY	661	DAVLENTAVAEVAMAYSGDSLSDNEKLYTLDYKMAEELIVSGAHLAIKOMAGLR	720	CC
Db	661	DAVLENTAVAEVAMAYSGDSLSDNEKLYTLDYKMAEELIVSGAHLAIKOMAGLR	720	CC
QY	601	DREAMPVNNTOMLRLQRNTVGTYPDSVCRFVKAASSGVDIFRIFDMLNDYSQMRPA	660	CC
Db	601	DREAMPVNNTOMLRLQRNTVGTYPDSVCRFVKAASSGVDIFRIFDMLNDYSQMRPA	660	CC
QY	661	DAVLENTAVAEVAMAYSGDSLSDNEKLYTLDYKMAEELIVSGAHLAIKOMAGLR	720	CC
Db	721	PAAVKLVLTARREDFLPVWHTHTAGGDLATYFAAOAGADAVGASAPLSGTQS	780	CC
Db	721	PAAVKLVLTARREDFLPVWHTHTAGGDLATYFAAOAGADAVGASAPLSGTQS	780	CC
QY	781	LSAIVAAFAATPRDQGLSLAEVDIPEPYEAVRGYLPLPESGTCPPTGRVYRHELPGCOL	840	CC
Db	781	LSAIVAAFAATPRDQGLSLAEVDIPEPYEAVRGYLPLPESGTCPPTGRVYRHELPGCOL	840	CC
CC	analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a mutant protein described in the exemplification of the invention.			
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.			
XX	Sequence 1140 AA;			
SQ				
Query	Match	99.9%; Score 5780; DB 22; Length 1140;		
Bast	Local Similarity	99.9%; Pred. No.: 0; Mismatches: 1; Indels: 0; Gaps: 0;		
Matches	1139; Conservative			

Db	558	FRDAHQSSLATRVSFALKPAAEAVAKLTPPELSVEANGGATDVAMRFLEFWDRIDE	617	XX	Proteins and their DNA useful for microbial production of L-amino acids
QY	601	LREAMPNVIQMLLRGRNIVGTYDPSDCRAFYKEAASSGVDFRIFRDALNDVSQMRPA	660	PT	-
Db	613	LREAMPNVIQMLLRGRNIVGTYDPSDCRAFYKEAASSGVDFRIFRDALNDVSQMRPA	677	XX	Claim 9; Page 132-135; 215pp; Japanese.
QY	661	IDAVLENTNAAEYAMASGDSLDPNEKXLTDLYKMAEETVKGSAHILAKDMAGLRR	720	XX	The present sequence is provided in a specification relating to genes
Db	673	IDAVLENTNAAEYAMASGDSLDPNEKXLTDLYKMAEETVKGSAHILAKDMAGLRR	737	CC	encoding thermophilic amino acid biosynthesis system enzymes of
QY	721	PAAVTKLYVALRREFDLPVPHVHTHDATAGGQATYFAAQAGADAVDGASSAPLGTTSQPS	780	CC	the thermotolerant bacterium <i>Corynebacterium</i> thermomaminogenes.
Db	738	PAAVTKLYVALRREFDLPVPHVHTHDATAGGQATYFAAQAGADAVDGASSAPLGTTSQPS	797	CC	The novel proteins retain at least 30% isocitrate ligase activity
QY	781	LSATVAARAHTRRDTGSLSEAVSDELPWWEAVRGLYLPFESGTGGPTGRVYRHEPGSQL	840	CC	enzymes were isolated from a <i>Corynebacterium</i> thermomaminogenes
Db	798	LSATVAARAHTRRDTGSLSEAVSDELPWWEAVRGLYLPFESGTGGPTGRVYRHEPGSQL	857	CC	chromosomal DNA plasmid library by PCR. The DNA may be used for
QY	841	SNRQAQATLGLADRFELIEDNTAAVNMLGRPTKVPSSKGVDLALHLYAGVDPDF	900	CC	developing strains of amino acid producing microorganisms.
Db	858	SNLRAQATLGLADRFELIEDNTAAVNMLGRPTKVPSSKGVDLALHLYAGVDPDF	917	XX	XX
QY	901	AADPOKYDIPDSVTAFLRGELNPGGMPPEPRLTRALEGRSGEKAPLTYPEEEQAHDA	960	CC	Sequence 1139 AA;
Db	918	AADPOKYDIPDSVTAFLRGELNPGGMPPEPRLTRALEGRSGEKAPLTYPEEEQAHDA	977	CC	Query Match 91.6%; Score 5302.5; DB 22; Length 1139;
QY	961	DDSKERRNSLNLFLPKPTEEFLEHRRRGNTSALDREFEFGVLNEGRETLRLPDVTP	1020	QY	Best Local Similarity 91.0%; Pred. No. 0; Matches 1036; Conservative 43; Mismatches 58; Indels 1; Gaps 1;
Db	978	DDSKERRNSLNLFLPKPTEEFLEHRRRGNTSALDREFEFGVLNEGRETLRLPDVTP	1037	Db	3 THRSSTLPFAKKLIVANRGEIAVRAFRAALETGAATVAVIYPREDFRSFRHRSFAEVRIG 62
QY	1021	LLVRDAAISEPDGKMRANAVANINGQIRPMYRDRVSVESTVAAEKADSNSKGHVAAPFA	1080	QY	3 TRPSTPFAKKLIVANRGEIAVRAFRAALETGAATVAVIYPREDFRSFRHRSFAEVRIG 62
Db	1038	LLVRDAAISEPDGKMRANAVANINGQIRPMYRDRVSVESTVAAEKADSNSKGHVAAPFA	1097	Db	123 LTGDKSKRASVAAKKAGLFLVLAESTPSKNDIETVSKAAGQTYPIFVAVAGGGGRMRFVA 182
QY	1081	GVVTVTVAEGDEVKAGDAWAITEAMKHEATIPASVCKIDRVWPAATKVEGDLIVWS	1140	QY	123 LTGDKSKRASVAAKKAGLFLVLAESTPSKNDIETVSKAAGQTYPIFVAVAGGGGRMRFVA 182
Db	1098	GVVTVTVAEGDEVKAGDAWAITEAMKHEATIPASVCKIDRVWPAATKVEGDLIVWS	1157	Db	183 SDEELRKLATEASREAAFAFGDGAVERAVINPOHEVOTLGHDGEVWHLYERDCSLO 242
RESULT 10				QY	183 SDEELRKLATEASREAAFAFGDGAVERAVINPOHEVOTLGHDGEVWHLYERDCSLO 242
AAB83180				QY	243 RRHKQVVEIAPAQHUEPELRICADAVFKCRSIGQAGATEFLDEKGHNHFEMNPR 302
ID AAB83180		standard; Protein; 1139 AA.		Db	243 RRHKQVVEIAPAQHUEPELRICADAVFKCRSIGQAGATEFLDEKGHNHFEMNPR 302
AC AAB83180;				QY	303 IQEVEHTVTEEVTDVLYKAQMLAAGATKELKGILTQDKIKTHGAALQCRITTEDPNNGR 362
XX				Db	303 IQEVEHTVTEEVTDVLYKAQMLAAGATKELKGILTQDKIKTHGAALQCRITTEDPNNGR 362
DT 09-JUL-2001 (first entry)				QY	363 PDTGTGTTAYRSPGGAVYRLDGAQOLGEGETAHFDSDMVKMCRGSDPFTVARAQRALAE 422
XX				Db	363 PDTGTGTTAYRSPGGAVYRLDGAQOLGEGETAHFDSDMVKMCRGSDPFTVARAQRALAE 422
DE Corynebacterium thermoaminogenes pc protein.				QY	423 FTVSGVATNIGFLRALLREEDFTSKRATGTFIADHFLQAPPADEGQGRIDLVDATV 482
XX				Db	423 FTVSGVATNIGFLRALLREEDFTSKRATGTFIADHFLQAPPADEGQGRIDLVDATV 482
OS Corynebacterium thermoaminogenes.				QY	483 NPKPHGRPKDVAAPIDKLPNPKDLPPLPRGSRDRDLQKQGPAFARDLREQDQALAVDTTFR 542
XX				Db	483 NPKPHGRPKDVAAPIDKLPNPKDLPPLPRGSRDRDLQKQGPAFARDLREQDQALAVDTTFR 541
PN WO200125447-A1.				QY	543 DAHQSLATRVSFALKPAAEAVAKLTPPELSVEANGGATDVAMRFLEFWDRIDE
XX				Db	542 DAHQSLATRVSFALKPAAEAVAKLTPPELSVEANGGATDVAMRFLEFWDRIDE
PD 12-APR-2001.				QY	542 DAHQSLATRVSFALKPAAEAVAKLTPPELSVEANGGATDVAMRFLEFWDRIDE
XX				Db	542 DAHQSLATRVSFALKPAAEAVAKLTPPELSVEANGGATDVAMRFLEFWDRIDE
PF 04-OCT-2000; 2000WO-JP06913.				QY	603 EAMPNVNIQMLLRGRNIVGTYDPSDCRAFYKEAASSGVDFRIFRDALNDVSQMRPAID 662
XX				Db	602 EAMPNVNIQMLLRGRNIVGTYDPSDCRAFYKEAASSGVDFRIFRDALNDVSQMRPAID 661
PA (AJIN) AJINOMOTO CO INC.				QY	663 AVLENTNAAEYAMASGDSLDPNEKXLTDLYKMAEETVKGSAHILAKDMAGLRR 722
XX				Db	662 AVLENTNAAEYAMASGDSLDPNEKXLTDLYKMAEETVKGSAHILAKDMAGLRR 721
PI Hirano S, Nonaka G, Matsuzaki Y, Akiyoshi N, Nakamura K, Kimura E;				QY	723 AVTKLYVALRREFDLPVPHVHTHDATAGGQATYFAAQAGADAVDGASSAPLGTTSQPSMS 782
PI Osumi T, Matsui K, Kawahara Y, Kurahashi O, Nakamatsu T;				Db	722 AVPKLYVALRREFDLPVPHVHTHDATAGGQATYFAAQAGADAVDGASSAPLGTTSQPSMS 781
XX Sugimoto S;					
DR WPI; 2001-3-300170/31.					
DR N-PSDB; AF87437.					
“					

Db	378	FRPDGQTATRSPGAGVRLGAGAQLGGEITAHDSDMLVKMTCRGSDFETAVARQRAL 437
Db	421	AETFTSGVATNIGFERALLRBDFFSKRATGFTADPHLQAPPADDEGRRILLYLADY 480
Db	438	AEFTSGVATNIGFERALLRBDFFSKRATGFTADPHLQAPPADDEGRRILLYLADY 497
QY	481	TVNKHGIVPRKDVAAPIDKLPLNIKOLPLPGRSDR 515
Db	498	TVNKHGIVPRKDVAAPIDKLPLNIKOLPLPGRSDR 532
RESULT 12		
AAU0511		AAU0511 standard; Protein; 1148 AA.
XX		
AC	AAU0511;	
XX		
DT	07-SEP-2001	(first entry)
XX		
DE	Bacillus subtilis	pyruvate carboxylase enzyme A.
XX		
KW	Pyruvate carboxylase A; pyCA; oxaloacetate; Escherichia;	L-amino acid production; fermentation.
XX		
OS	Bacillus subtilis	strain 168.
XX		
EP1092776-A1.		
PA		(AJIN) AJINOMOTO CO INC.
PD		18-APR-2001.
XX		
PF		05-OCT-2000; 2000EP-0121763.
XX		
PR		14-OCT-1999; 99RU-0121636.
XX		
PA		(AJIN) AJINOMOTO CO INC.
XX		
PI	Gusyatiner MM, Kozlov YI, Ptitsyn LR, Altman IB, Voroshilova EB;	
PT	PI	Yamontas YAV, Yampolskaya TA;
XX		
DR	WPI: 2001-309819-33.	
XX		
PS	Claim 4; Page 17-21; 28pp; English.	
XX		
PT	New bacterium from the genus Escherichia containing a gene encoding for	
PT	pyruvate carboxylase useful for producing higher concentrations of	L-amino acids
XX		
PS	Claim 4; Page 17-21; 28pp; English.	
XX		
CC	The present sequence represents <i>Bacillus subtilis</i> pyruvate	
CC	carboxylase enzyme A. The pyCA gene encodes for pyruvate carboxylase	which catalyses the carboxylation of pyruvate to form oxaloacetate.
CC	Transformation of the <i>Bacillus subtilis</i> pyCA gene into a bacterium	belonging to the genus <i>Escherichia</i> results in the bacterium showing
CC	L-amino acid productivity. The invention provides a novel method for	producing an L-amino acid by fermentation. The method involves
CC	cultivating the bacterium in a medium and producing and accumulating	the L-amino acid in the medium. The new bacterium harbouring the gene
CC	coding for an enzyme having pyruvate carboxylase activity is useful	for producing higher concentrations of L-amino acids in vitro than
CC	prior art.	
XX		
SQ	Sequence	1148 AA;
Query Match	43.6%	Score 2524; DB 22; Length 1148;
Best Local Similarity	46.0%	Score 2524; DB 22; Length 1148;
Matches	533; conservative	186; Mismatches 392; Indels 48; Gaps 13;
QY	11	AEFTSGVATNIGFERALLRBDFFSKRATGFTADPHLQAPPADDEGRRILLYLADY 70
Db	5	SIOKVLVANRGEAIRFRACTELNLIRTVAVVSKEDSGSYHRYKADEAYLVGEGKPIDA 64
QY	71	YLVDEDEIGAKKVKADAIYPGFGFSENQARCAENGIFIGPPPEVLDITGDKSRA 130
Db	65	YLDIEGIDIAKRNKYDAIHPGYGFSENIRFARCEEGIVFIGPKSEHLDGMFGDKVA 124
QY	131	YTAKKAGLPLVLAEST-PSKIDELVKSACQTYPIFVKAVAGGGGRGMREVASDELK 189
Db	125	RESQARAGTIP-IPGSDGPAELAVSQFGQNGYPTIKASLGGGRGMREVSEKEVE 184
QY	190	LATEASREAAAFGDAVYVERAVINPOHIEVQILGDHTGEVWHLKERDGSILQRHQKV 249
Db	185	AYERANSEAKAAGFNGEDEVVYKLEINPKHIEVQIGDQKQGVHFLERODSVQRHHOKV 244
QY	250	ETAPAOHLDPELDRITCDAVAKFCRSIGYQAGTYFLVDEKGHNFIEMPRIOVENT 309
Db	245	EVAPSVLSPLEIRPQDICEAAVALAKNVINYNGTVEFLV ANNEYFIEVNPVROVENT 303
QY	310	TEEVTEVDLVAOMRLLAAGAYL-KIGLGLDK-ITKTHGAALOCRITTEPPNNGRPDTG 366
Db	364	KIMAYRSGGGFGVRDGTGNSHOGAVITPYDSSLVVKLSTWALTEBQAAKMRVNQEFERI 423
QY	426	SGWATNIGFLERALLREEDFTSSKRATGFIADPHLQAPPADDEGRRILLYLADYVN- 483
Db	304	TEMITGVDIVOTQOLVAGQHSLSHSKVNIPTEQDQDIFTGTAQISRVTEPDONDMPDTG 363
QY	367	TITAVRSPGGGVRLD-GAQOLGGETAHDSDMLVKMTCRGSDFETAVARQRALAEFTV 425
Db	424	PGKININPFLLENVAKHEKFLGQYDTSIDTPELFENPKQDKRGTMLYIGNVTNGP 483
QY	484	-----KPHGVRPKVAAPIDKLPLPGRSDRDKLQLGPAAFARDLRSODALAV 536
Db	484	PGIGKEKPAEDPLKGVKVWDQQP-----ARGTKQILDEKGEGLEANLWNVKECKSVL 536
QY	537	TDTTERDAHOSLLATRVSFAALKPAEAVAKLPELSEVAWGGATYDAMRFEDPND 596
Db	537	TDTTFRDAHOSLLATRIRSHDLKKITANPTAAWPELFMSMWWGATFDAYRFLKEDPWN 596
QY	597	RDELEIRREAMVNQNLRLRRTVQYTPYFDSVCRFVKAASSGVDIRIFDALNDVSQ 656
Db	597	RLEDLKEVPTNLFOMLRLSSNAGVNTYDNPVNEKEFVQKOSGIDDVRFEDLSLNWKG 656
QY	657	MRPAIDAVLLENTAVAEVAMAYSGLDISDNEPKLYLDDYKKMAEPIVSKGAAHIAKDMA 716
Db	657	MTLAIDAVRTG-KYAAEATCYTGBDILKNRTKVDLAVTSMAKELEAAGHILGKDMA 715
QY	717	GLLRDAVTRKLVTALARREFDLPVHHTDAGGOLATYFAAQAGADAVDGASPLGTT 776
Db	716	GULKEFOAWEVLVSLAKETIDPVHLHTDTSNGNIMYAKAVERGVDIIVAVSSMAGLT 775
QY	777	SOPSIASIAVAAFAHRRDPLGLSLRASDJEPPWAVRGYIPLPFSGTCPGPTGRYRHELP 836
Db	776	SOPSIASGFYHAMEGNDRREPMNVGVELLSQYWSVRKYSEFSGMSKSPHTEYHEMP 835
QY	837	GGQLSNLRAQATAGLADRELIEDNAYAVNEVMGRPTVTPSSKWGLDLHLVYAGVD 896
Db	836	GGQYSNLQOQAKGVLGDRWNEVEMYRVDNMGDIVKVTTPSSKWGDMLAVNQNLT 895
QY	897	PADRADPKYDPSVIAFLRGLGEIQLGNPFGWPPLRTRALLEGRSEGKAPLTVPEE- 953
Db	896	EKDYEKGESSLPSWVLFKGIGOPHGPHEPPLKQKOE---PITVRGELLE 951
QY	954	-----EOAHLDDDSKERNRNLJFPKPTEELERRRGNTISALDREFF 1001
Db	952	PVSVEAIKEKFEKHNLETSD---QDQAVAYALPKVFTDVKWITESTGDISLUDTPFF 1007
QY	1002	YGLVEGRETILRPLDVTPLVRLDAISEPDDKGMRNTVANVNGOIRPMVRURSVEVT 1061
Db	1008	YGMILGEETEVETERGKT-LIVKLJISIGEPQPDATRVVYFELNGQPREWVKKIDESKSV 1066
QY	1062	ATAKADSDSNKGVHAAPPGAVVTVAE-GDEVKAGDAVAILEAMKMATIASVGDKID 1120
Db	1067	QERLKDRTNPISHAASMPGTIVKVLBAGTKVNGDHLMINAEKMETTVQPFSGTRK 1126
QY	1121	RVVWPAATKVEGGDLIVV 1139

Query Match 43.0%; Score 2488; DB 22; Length 1147; Best Local Similarity 45.2%; Nond. 4.9e-174; Matches 527; Conservative 192; Mismatches 384; Indels 62;

8Y 1056 SVESVTATAEKADSSNKGGHVAAPFAGWT-VTVAEGLKAGDRAYVLTIFAMKMEATITAS 1111

QY	1115	NYHTNANVKPKRADKSNSPHIGAQMPGSVTEKVSVGETVKANOPLITEAMKNETTIQAP	1119
Db	1120	FDGVHQVTVNGDTATGDLIEI	1144
RESULT 15			
AAU35213	AAU35213	standard; Protein: 1142 AA.	
XX	XX		
AC	AC		
XX	XX		
DT	13-FEB-2002	(first entry)	
XX			
DE	Enterococcus faecalis cellular proliferation protein #500.		
KW	Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.		
XX			
OS	Enterococcus faecalis.		
XX			
PN	WO200170955-A2.		
XX			
PD	27-SBP-2001.		
XX			
PF	21-MAR-2001; 2001WO-US09180.		
XX			
PR	21-MAR-2000; 2000US-191078P.		
PR	23-MAY-2000; 2000US-206848P.		
PR	26-MAY-2000; 2000US-207737P.		
PR	23-OCT-2000; 2000US-242518P.		
PR	27-NOV-2000; 2000US-253655P.		
PR	22-DEC-2000; 2000US-257931P.		
PR	16-FEB-2001; 2001US-269308P.		
PR			
PA	(ELT-) ELTRA PHARM INC.		
XX			
PT	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;		
PT	Yamamoto RT, Xu HH;		
XX			
DR	WPI; 2001-61145/70.		
DR	N-PSDB; AAS53072.		
XX			
PT	New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -		
PT			
PS	Example 3: Seq ID NO 10806; 511pp; English.		
PS			
CC	The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, <i>Staphylococcus aureus</i> , <i>Salmonella typhi</i> , <i>Klebsiella pneumoniae</i> , <i>Pseudomonas aeruginosa</i> and <i>Enterococcus faecalis</i> . The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.		
CC			
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at		
CC	ftp.wipo.int/pub/published_pct_sequences.		
XX			

Db 999 TFFNGIROGETLEVOIERTGKT-LIRLDIEGEPDIDGNRVLFFNINGQRREVLVKDASIK 1057
QY 1059 SVTATAEKADSSNKHVAAPFAG-VVTVTVAEGDEVKADDAVATEAMMKEATITASVDG 1117
Db 1058 SAVQVKQKAPTPNKEQIGAMMSGVILQVLVKRGDKVEKGOPPLITEAMMKTTEARFAG 1117
QY 1118 KIDRVVVPAAATKVEGGDLIVVV 1139
Db 1118 TVDHIVVEGEAISSGDLILIEV 1139

Search completed: September 24, 2003, 15:55:26
Job time : 68.5263 secs